Pretest Video Education Versus Genetic Counseling for Patients With Prostate Cancer: ProGen, A Multisite Randomized Controlled Trial

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ABSTRACT

PURPOSE Germline genetic testing (GT) is recommended for men with prostate cancer (PC), but testing through traditional models is limited. The ProGen study examined a novel model aimed at providing access to GT while promoting education and informed consent.

METHODS Men with potentially lethal PC (metastatic, localized with a Gleason score of ≥8, persistent prostate-specific antigen after local therapy), diagnosis age ≤55 years, previous malignancy, and family history suggestive of a pathogenic variant (PV) and/or at oncologist's discretion were randomly assigned 3:1 to video education (VE) or in-person genetic counseling (GC). Participants had 67 genes analyzed (Ambry), with results disclosed via telephone by a genetic counselor. Outcomes included GT consent, GT completion, PV prevalence, and survey measures of satisfaction, psychological impact, genetics knowledge, and family communication. Two-sided Fisher's exact tests were used for between-arm comparisons.

RESULTS Over a 2-year period, 662 participants at three sites were randomly assigned and pretest VE (n = 498) or GC (n = 164) was completed by 604 participants (VE, 93.1%; GC, 88.8%), of whom 596 participants (VE, 98.9%; GC, 97.9%) consented to GT and 591 participants completed GT (VE, 99.3%; GC, 98.6%). These differences were not statistically significant although subtle differences in satisfaction and psychological impact were. Notably, 84 PVs were identified in 78 participants (13.2%), with *BRCA1/2* PV comprising 32% of participants with a positive result (*BRCA2* n = 21, *BRCA1* n = 4).

CONCLUSION Both VE and traditional GC yielded high GT uptake without significant differences in outcome measures of completion, GT uptake, genetics knowledge, and family communication. The increased demand for GT with limited genetics resources supports consideration of pretest VE for patients with PC.

ACCOMPANYING CONTENT

Appendix

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INTRODUCTION

The identification of germline pathogenic variants (PVs) is integral to informing the treatment of prostate cancer (PC), as targeted therapy with poly (ADP-ribose) polymerase (PARP) inhibitors is approved for patients with homologous recombination deficiency (HRD) metastatic PC (mPC).[1,2] While 12% of PC cases are associated with PVs,[3] systematic processes to identify germline PVs have been limited and few studies have included cancer types beyond breast, ovarian, and colorectal cancers. With an estimated 288,300 new cases of PC in 2023,[4] it is imperative to identify additional service delivery models to meet the increasing demand for timely access to genetic testing (GT).

Despite the well-established benefits of GT for patients with cancer including informing treatment, screening, and cascade testing of family members, there has been inconsistent

CONTEXT

Key Objective
How does pretest video education (VE) on germline genetic testing (GT) compare with traditional genetic counseling for patients with prostate cancer (PC)?

Knowledge Generated
In this randomized controlled clinical trial of 662 patients with PC, there were no statistically significant differences between arms in uptake of GT, knowledge of GT, or family communication of results. There were some differences in satisfaction and psychological impact.

Relevance
Overall, given the increased demand for GT with limited genetics resources, pretest VE is a valuable platform for facilitating GT, although further study is needed.

integration of germline genetics into oncology workflows, leading to significant gaps in care.[5,6] Rates of cancer genetic counseling (GC) are unacceptably low (approximately 20%) among individuals with standard or guideline-based indications for GT within integrated health care systems,[7,8] commercially insured patients,[9] and minorities.[10-13] Barriers to GT include long wait times and uneven access to genetics experts.[14-16] Despite clear clinical guidelines recommending universal testing for an expanding number of cancers,[8,17-19] GC resources are not well matched to clinical needs among patients with a high probability of carrying a germline PV.[20,21] In fact, genetics professionals have cited the shortage of providers as one of the biggest challenges in the field.[22]

Digital health technologies may represent an opportunity to combat this problem and perform scalable genetic assessments as indications for GT continue to increase. At the time this trial was designed, while the importance of GT for patients with PC was anticipated on the basis of the high PV prevalence,[3] little data on alternatives to in-person GC services existed. Randomized trials comparing traditional with alternative and streamlined delivery approaches, including those conducted by our group, have consistently shown comparable or noninferior outcomes among patients with cancer.[23-28] PVs in *BRCA2* are known to be implicated in the development of early-onset and aggressive PC. Furthermore, cancer-specific survival is significantly worse in those with *BRCA* PVs compared with those without (median survival 8.6 years *v* 15.7 years).[29] PVs in HRD genes like *BRCA2* and mismatch repair (MMR) genes, among others, have treatment implications. A novel and efficient genetics service delivery model for patients with PC will have significant clinical implications for GC, testing, and targeted treatment, with the goal of ultimately improving survival for patients with PC.

The primary aim of this study was to assess uptake of GT in patients with PC in a randomized trial of pretest video education (VE) compared with in-person GC and to measure satisfaction, distress, and knowledge by randomized arm.

METHODS

Participants

From January 2017 through December 2019, patients were recruited for a randomized controlled trial evaluating in-person, pretest VE or GC from three sites: Dana-Farber Cancer Institute (DFCI, Boston, MA), University of Texas Southwestern Medical Center (Dallas, TX), and Karmanos Cancer Institute (Detroit, MI). Eligible patients were English-speaking and age ≥18 years, with one of the following criteria: mPC (hormone-sensitive, de novo, or castration-resistant [mCRPC]); localized PC with a Gleason score of ≥8; rising prostate-specific antigen (PSA) level after prostatectomy or radiation; persistent PSA after prostatectomy; PC at age ≤55 years; any PC with a personal history of other malignancy, or biopsy with high-grade prostatic intraepithelial neoplasia, or small acinar proliferation; and/or cancer family history (CFH) potentially indicating a germline PV (eg, premenopausal breast cancer, cancers of the ovary, pancreas, and colorectum, in ≥1 first- or second-degree relatives). Patients were excluded if they had previous cancer GC or GT, active hematologic malignancy, or localized PC previously treated and in remission for ≥2 years without CFH.

Procedures

Institutional review board approval was obtained at all study sites. The VE was developed by a team of cancer genetic counselors (CGCs), geneticists, and medical oncologists who wrote the script for narration (ninth-grade reading level), created a storyboard, and provided accompanying visuals (graphic representations of DNA, pedigree, consent form, test report, and illustrative imagery). Production was iterative as feedback was incorporated from the lay community. The final video was a professionally produced, 8-minute summary of the key educational components of a cancer

GC visit including the choice in GT, the role of genes in cancer, multigene panel testing, psychosocial implications of testing, genetic discrimination, inheritance patterns, types of results, cascade testing, screening, prevention, and treatment implications.[30,31]

Eligible patients were identified through their medical oncologist or through the cancer genetics practice at each site. Of the 784 eligible patients approached by study coordinators, 662 (84%) consented to study participation. Data were not collected on nonconsenting patients. Consented patients were randomly assigned 3:1 to pretest VE or in-person GC (Fig 1). Random assignment occurred through a central process managed by the Office of Data Quality at DFCI, with stratification by hormone-sensitive/castrate-resistant PC. Per standard clinical practice, CFH was collected via a secure link to an electronic family history questionnaire. The CFH was reviewed and updated at the time of their visit for participants randomly assigned to the GC arm and at the time of result disclosure by a CGC for participants in the VE arm.

Intervention

The GC arm consisted of a traditional in-person pretest visit with a CGC (standard of care), in which the participant typically spent 30-45 minutes discussing their CFH, the potential impact of identifying inherited cancer risk for themselves and their family, and the benefits, risks, and limitations of GT. On the VE arm, a research coordinator (RC) played the VE for the participant on an iPad in a designated clinic space (consultation or examination room). Participants were offered the opportunity to consent to GT by the CGC or RC (depending on arm) at the end of their visit. Participants in the VE arm could request access to a CGC at any time.

Participants were consented to GT of 67 genes (Appendix, online only) through Ambry Genetics, and interpretation of sequence variations was performed according to the American College of Medical Genetics and Genomics guidelines.[32] Both PVs and likely PVs were denoted as PVs for analysis in this study.

Insurance was billed for the GT, and out-of-pocket costs were waived to avoid biasing study end points. Participants on both arms, irrespective of the test results, received their result via telephone disclosure by a CGC (standard of care). Those with a PV were encouraged to follow-up in clinic with a CGC and cancer genetics physician.

Measures and Statistical Analyses

The study was designed with 3:1 random assignment of 660 participants to account for an estimated 10% attrition, cost savings, greater power to detect between arm differences, and smaller confidence intervals. Although a noninferiority design for the primary end point was considered, it was not selected because of feasibility and to identify superiority of either arm if present. Demographic information, PC characteristics, CFH, and outcomes, including consent to and completion of GT, were tabulated. Forward stepwise logistic regression was performed with two separate outcome variables: all PV results and *BRCA1/2* only PV results, with relevant clinical and demographic variables as covariates.

Survey measures for secondary outcomes collected at or shortly after the time of intervention included Result Disclosure Survey and an adapted version of the previously validated Genetic Testing Satisfaction Survey (GTSS).[33] All analyses of surveys administered after the disclosure of GT results were performed separately for those with and without PVs. At 1 month after result disclosure, the GTSS was repeated (GTSS2) and the Multidimensional Impact of Cancer Risk Assessment (MICRA)[34,35] and Family Communication Survey (FCS) were administered. The FCS was administered to participants with a PV only. The KnowGene scale, a validated measure of knowledge of cancer multigene panel testing, was delivered 4 months after the result disclosure[36] (Appendix).

RESULTS

From January 2017 through December 2019, 662 patients consented to the study. The median age at study entry was 66 years with a range of 40-86 years, and at PC diagnosis, it was 61 years with a range of 39-82 years. Most participants were White (88%), 40% had mPC, and 74% had castrate-resistant PC. Baseline participant characteristics by arm were similar (Table 1).

Uptake and Genetic Test Results

Of the 662 randomly assigned participants 605 (91.4%) completed their randomized intervention assignment (GC or VE), 597 (90.2%) consented to GT, and 593 (89.5%) completed testing with no statistically significant differences by arm. Of the 498 participants randomly assigned to the VE arm, 461 (93%; 95% CI, 90 to 95) completed the VE visit; of those, 456 (99%; 95% CI, 98 to 100) consented to GT, of whom 453 (99.3%; 95% CI, 98 to 100) completed GT. Of the 164 participants randomly assigned to the GC arm, 144 (88% 95% CI, 82 to 92) completed GC visit; of those, 141 (98%; 95% CI, 94 to 100) consented to GT, of whom 140 (99.3%; 95% CI, 96.1 to 100) completed GT. Differences between arms were not statistically significant. Only five participants without PVs from the VE arm (approximately 1%) asked to speak with a GC.

Most participants had negative test results (n = 310, 52%); 203 participants had a variant of uncertain significance (34%). PVs (n = 84) were identified in 78 (13%) participants; an additional two participants had mosaic *NF1* results related to clonal hematopoiesis of indeterminate potential. *BRCA1/2* PV accounted for 32% of subjects with a positive result (*BRCA2*:21, *BRCA1*:4). PVs in other genes traditionally associated with breast and/or ovarian cancer were as follows: *CHEK2*, n = 8 (one co-occurring with monoallelic *MUTYH*); *ATM*, n = 5

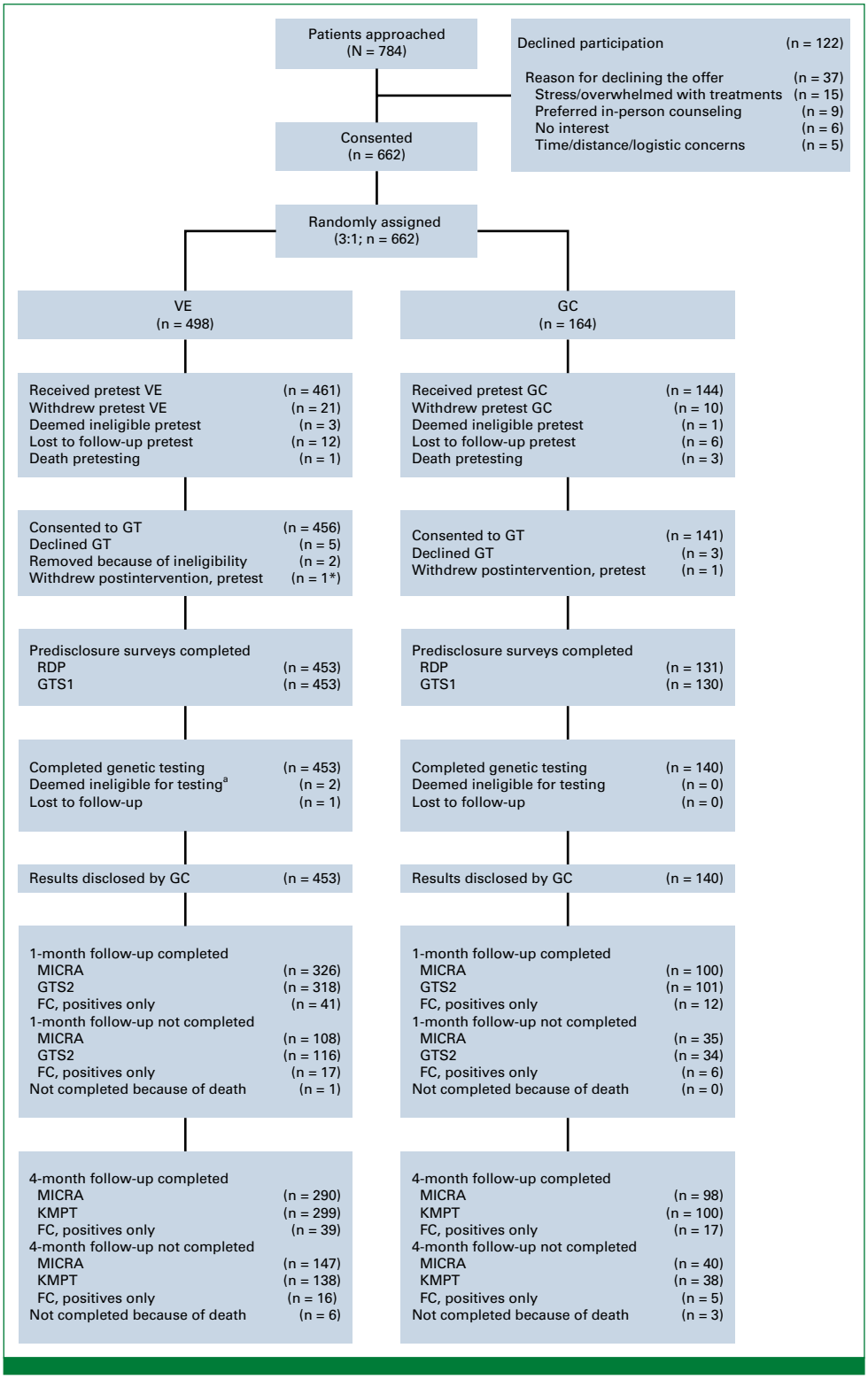

FIG 1. CONSORT diagram. FC, family communication; GC, genetic counseling; GT, genetic test; GTS1/2, Genetic Testing Satisfaction Survey at time point 1 and 2; KMPT, knowledge of multigene panel testing (KnowGene); MICRA, Multidimensional Impact of Cancer Risk Assessment; RDP, result disclosure; VE, video education.[a]chronic lymphocytic leukemia

(one co-occurring with *MRE11A*); *BARD1*, n = 2; *RAD50*, n = 2; *RAD51C*, n = 1; *RAD51D*, n = 1; and *NBN*, n = 1. PVs in the MMR were identified in *PMS2*, n = 3 (one co-occurring with *SDHC*); *MSH6*, n = 2; and *MLH1*, n = 1. Results included other PVs, the most frequent of which was monoallelic *MUTYH*, n = 9 (Table 2).

TABLE 1. Participant Demographics

Characteristic	GC (n = 164)	Video (n = 498)	Overall (N = 662)
Age at prostate cancer diagnosis, years			
Median (IQR)	61 (54-66)	60 (55-66)	61 (55-66)
Range	39-81	40-82	39-82
Age at study enrollment, years			
Median (IQR)	66 (60-71)	67 (59-72)	66 (60-71)
Range	42-86	40-84	40-86
Self-reported race/ethnicity/ancestry, No. (%)			
Ashkenazi Jewish			
Yes	12 (7)	42 (8)	54 (8)
Uncertain	19 (12)	61 (12)	80 (12)
Ethnicity			
Asian	1 (<1)	6 (1)	7 (1)
Black	8 (5)	25 (5)	33 (5)
Hispanic or Latinx	1 (<1)	1 (<1)	2 (<1)
White	142 (87)	443 (89)	585 (88)
Others	9 (5)	13 (3)	22 (3)
Multiple	2 (1)	9 (2)	11 (2)
Declined to answer	1 (<1)	1 (<1)	2 (<1)
Gleason score			
6	22 (13)	41 (8)	63 (10)
7	46 (28)	140 (28)	186 (28)
≥8	91 (55)	292 (59)	383 (58)
NA	5 (3)	25 (5)	30 (5)
Disease status			
Localized	102 (62)	297 (60)	399 (60)
Metastatic	62 (38)	201 (40)	263 (40)
Stratification			
Hormone-sensitive	44 (27)	129 (26)	173 (26)
Castration-resistant	120 (73)	369 (74)	489 (74)
Cancer family history			
Prostate only	45 (27)	110 (22)	155 (23)
Breast with or without ovarian with or without pancreatic with or without prostate	23 (14)	57 (11)	80 (12)
Colorectal with or without uterine with or without prostate	15 (9)	36 (7)	51 (8)
Recruitment site			
DFCI	147 (89)	442 (89)	589 (89)
Karmanos	11 (7)	34 (7)	45 (7)
University of Texas Southwestern	6 (4)	22 (4)	28 (4)

Abbreviations: DFCI, Dana-Farber Cancer Institute; GC, genetic counseling; NA, not available.

Survey Results

Satisfaction

Response rates to GTSS1 (completed immediately after completion of the intervention, before genetic test results) were 99% for VE and 95% for GC. After correcting for multiple comparisons, agreement on one question ([my genetic counselor/the video] answered all my questions and concerns) was found to be significantly different ($P < .001$) between the VE and GC arms using a Fisher's exact test (Fig 2A) with results favoring the GC arm.

On the GTSS2 (completed 1 month after result disclosure), among participants with no PV (VE, n = 276; GC, n = 87), agreement was found to be significantly different ($P < .001$) between arms on the same question as GTSS1 above again, favoring GC (Fig 2B). However, for participants with PVs (VE, n = 42; GC, n = 12), there was less anxiety with VE ($P = .005$) on the basis of the question ("The information presented by [my genetic counselor/the video] was worrisome or anxiety inducing"; Fig 2C).

Analysis of differences in answers item by item was conducted for results of the GTSS1 and GTSS2 for 413 participants, 317

TABLE 2. Germline GT Results

Gene	PV Count	n = 593 (%)	n = 78 (%)
APC	4	0.7	5
ATM	4	0.7	5
ATM and *MRE11A*	1	0.2	1
BARD1	2	0.3	3
BRCA1	3	0.5	4
BRCA1 and *XRCC2*	1	0.2	1
BRCA2	19	3.2	24
BRCA2 and *APC*	1	0.2	1
BRCA2 and *MITF*	1	0.2	1
CHEK2	7	1.2	9
CHEK2 and *MUTYH* (monoallelic)	1	0.2	1
FANCC	2	0.3	3
FH	4	0.7	5
HOXB13	4	0.7	5
MITF	3	0.5	4
MLH1	1	0.2	1
MSH6	2	0.3	3
MUTYH (monoallelic)	8	1.4	10
NBN	1	0.2	1
PMS2	2	0.3	3
PMS2 and *SDHC*	1	0.2	1
POT1	1	0.2	1
RAD50	2	0.3	3
RAD51C	1	0.2	1
RAD51D	1	0.2	1
SDHA	1	0.2	1

NOTE. Of participants with genetic testing results (n = 593), 78 patients had a total of 84 PVs or likely PVs. Note that six participants had two PVs each, and these are tabulated as pairs and are not included into the total of each single gene.
Abbreviations: GT, genetic test; PV, pathogenic variant.

(69%) on the VE arm and 96 (67%) on the GC arm using a Fisher-Freeman-Halton test and a Holm's correction for multiple comparisons. Among participants with no PV, there was a significant difference ($P < .01$) in responses between GTSS1 and GTSS2 as to whether all the participants' questions and concerns had been addressed by their intervention favoring GC.

Psychological Impact

Between-arm differences in the total MICRA score from 1-month post–result disclosure were not statistically significant among participants with PVs. For participants with no PV, the total MICRA score was higher (worse) in the GC arm ($P = .02$; Fig 3A). Analysis of MICRA subscales by test result found greater distress among participants with PVs in the GC arm ($P = .05$; Fig 3F) and greater positive experiences among participants with no PV ($P = .04$) in the GC arm (Fig 3C).

At 4 months postdisclosure, the total MICRA score was not significantly different between the VE and GC arms for participants with or without PVs. The only significant difference in evaluating the subscales was that among participants with a PV, those in the GC arm had more positive experiences ($P = .01$; Fig 3O).

Differences between the total scores and subscales on the 1-month and 4-month MICRA surveys were evaluable for 340 participants who completed the survey at both timepoints (VE, 259; GC, 81; Appendix Table A1, online only). No statistically significant differences were found between the 1-month and 4-month MICRA among participants with a PV, whereas participants with no PV on the VE arm demonstrated more distress ($P < .01$) and less positive experiences ($P < .001$).

Knowledge

The KnowGene survey was completed by 305 participants on the VE arm (66% of those who completed the intervention) and 93 on the GC arm (65% of those who completed the intervention). The number of questions correctly answered was the outcome variable in a linear regression model with age at study entry (≤55, 55-65, ≥65 years), random assignment arm (VE *v* GC), PV (*v* no PV), and mPC (*v* nonmetastatic) as covariates. None of the covariates were found to be significant, and there were no significant differences in knowledge about multigene panel testing between the VE and GC arms (summary statistics in Appendix Table A2, online only).

Result Communication

Postintervention, 582 of 595 (98%) responded to the results disclosure survey. There was no difference in intent to disclose results to family members (VE, 99%; GC, 99%; Appendix Table A3, online only). Of 74 participants with PV results who received the FCS, 53 (72%) completed it and there were no significant differences in disclosing results to family (VE, 98%; GC, 100%; Appendix Table A4, online only).

DISCUSSION

GT is an important part of PC care and has been incorporated into the National Comprehensive Cancer Network Clinical Practice Guidelines in Oncology (NCCN Guidelines). There has been low compliance with GT for patients with breast or ovarian cancers, and it is anticipated that uptake in GT for patients with PC will be similarly low or lower.[37] Our results indicate that VE is a tool that can be used to expand the reach of limited resources and improve access to cancer GT. Patients with PC randomly assigned to VE or GC both had high levels of GT uptake with slightly better, though nonsignificant, uptake and completion in VE. Both VE and GC demonstrated high satisfaction after their intervention. These findings suggest that for patients with PC, pretest VE without pretest GC can be used to facilitate GT.

Developing testing strategies and infrastructure to maximize identification with germline PVs is especially important in

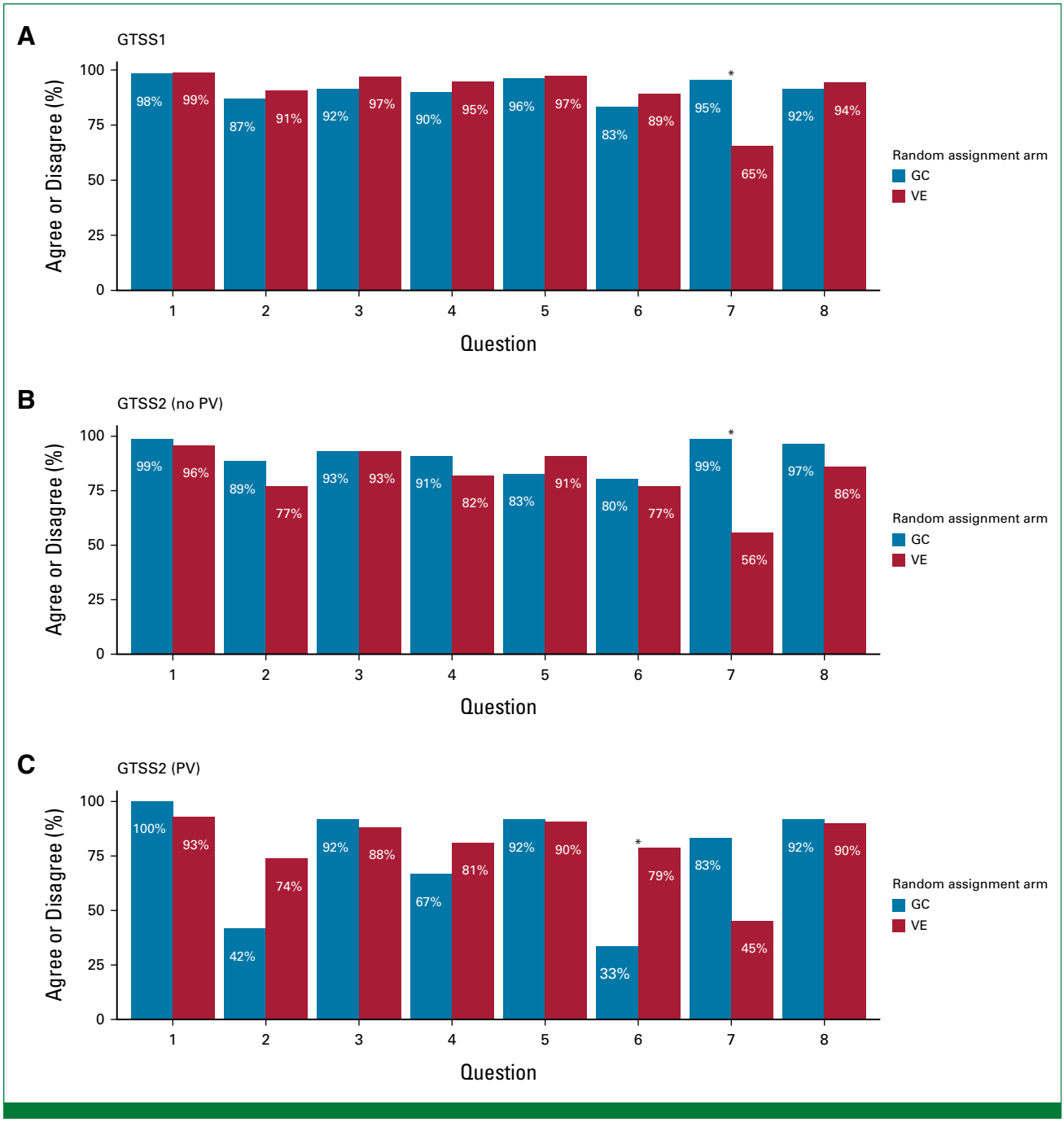

FIG 2. GTSS1 and GTSS2 survey responses. (A) On the VE arm, 65% (95% CI, 61 to 70) of respondents agreed with question 7, and on the GC arm, 95 (95% CI, 90 to 98) of respondents agreed with the statement. (B) On the VE arm, 56% (95% CI, 50 to 62) of respondents agreed with question 7, and on the GC arm, 99% (95% CI, 94 to 100) of respondents agreed with the statement. (C) On the VE arm, 79% (95% CI, 63 to 90) of subjects disagreed with question 6, whereas 33% (95% CI, 10 to 65) of respondents disagreed on the GC arm. Q1. The information presented by (my genetic counselor/the video) was informative. Q2. The information presented by (my genetic counselor/the video) was sad or depressing. Q3. The information presented by (my genetic counselor/the video) was confusing or difficult to understand. Q4. The information presented by (my genetic counselor/the video) was distressing. Q5. The information presented by (my genetic counselor/the video) was useful. Q6. The information presented by (my genetic counselor/the video) was worrisome or anxiety inducing. Q7. (My genetic counselor/the video) answered all of my questions and concerns. Q8. (My appointment with my genetic counselor/the video) was about the right length of time. *$P \leq .05$. GC, genetic counseling; GTSS, Genetic Testing Satisfaction Survey; PV, pathogenic variant; VE, video education.

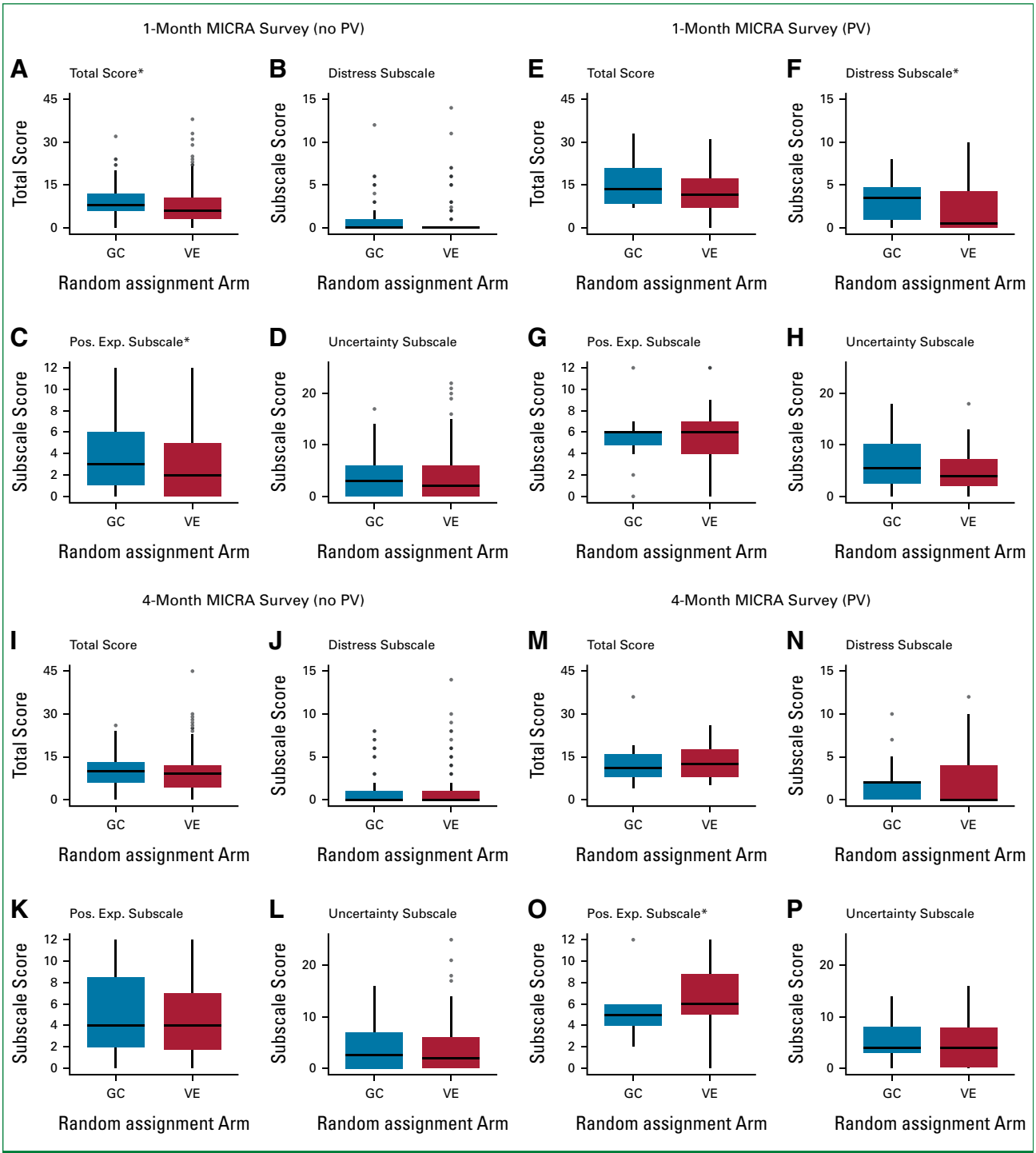

FIG 3. MICRA survey responses. Among participants with no PV (A-D, I-L), the 1-month total score (A) and the positive experience scales (C) differed by arm. Among participants with a PV (E-H, M-P), the distress subscale (F) at 1-month and the positive experience subscale at 4 months (O) differed by arm. *$P \leq .05$. GC, genetic counseling; MICRA, Multidimensional Impact of Cancer Risk Assessment; Pos. Exp., positive experiences; PV, pathogenic variant; VE, video education.

individuals with PC, given the high proportion of HRD genes attributed to PC predisposition. For example, *BRCA2* PVs were the most frequent PVs identified in this study (accounting for 2.7% of mPC cases, 3.5% of the tested participants, and 25% of PVs), a finding that has considerable therapeutic implications as PARP inhibitors have been FDA-approved for the treatment of *BRCA*+ mCRPC.[1,38,39] The *BRCA2* PV frequency is lower than that reported by Pritchard et al, in which 5.3% of patients with mPC had a germline BRCA2 PV; our cohort was purposefully not limited to mPC, thus accounting for some

differences.[3] The germline PV spectrum has important management implications.

The psychological outcomes associated with the different pretest approaches were mixed. After result disclosure, participants with PVs who had been in the GC arm had greater distress (at 1 month), but not at 4 months. Participants with no PVs who had been in the GC arm had greater satisfaction specifically with having their questions answered, more positive experiences, and less distress. This finding is not surprising given the tailored, expert communication and empathic exchanges that patients experience with CGCs.[25,40] However, only 1% of participants without PVs assigned to VE elected to meet with a CGC post-test despite ample opportunity to do so. Together with the fact that knowledge scores were not compromised in the VE arm, this low uptake of post-test GC may inform the prioritization of GC resources toward supporting patients and families with PVs. A noninferiority four-arm randomized trial of online cancer GT (MAGENTA) assessing the need for individualized pre- or post-test GC found no significant differences in anxiety, depression, or decisional regret in the arms in which pre- and/or post-test GC was omitted as compared with the control arms. Differences in our findings may be explained by study design as interventions were in person (not online) or by study population as our participants were markedly different from the MAGENTA population (males, all had cancer and were approximately 20 years older).[25,40]

Results from a nonrandomized, patient choice study of patients with PC found no differences in uptake of GT, knowledge, or decision regret with GT between VE and GC, and when offered a choice, patients selected VE.[41] This study, together with our data, demonstrates that a truncated approach to GT for this population is reasonable, in particular, as the identification of germline PV has become increasingly important for estimating prognosis and for treatment selection in oncology care.[42] While we found that uptake, satisfaction, knowledge, and psychosocial impact were favorable in both VE and GC arms, opportunities for providing tailored and personalized support exist. For example, chatbots or relational agents, which provide an interactive platform, may mitigate these differences.

The high GT completion rates in this study indicate that patients participating in our randomized trial on GT processes are a subset of patients with PC and, in practice, lower GT uptake may occur. Testing uptake would likely be lower in patients without cancer, especially among those with Medicare as the lack of coverage is often a barrier to GT access. Oncologic indications can mitigate some barriers as demonstrated in a study of pharmacogenomic GT among Medicare-enrolled individuals.[43] Despite the multisite approach designed to optimize participant geographic and racial diversity, the study population was mostly accrued at one site (DFCI) and therefore comprised predominantly White, English speakers in the United States limiting conclusions in other populations. This also introduces the potential bias of differences between patients who seek care at academic centers compared with community practices who may be more likely to seek novel or experimental diagnostic and treatment approaches. Response may be different with non-US patients and/or non-English speakers, which is the subject of an upcoming trial (ClinicalTrials.gov identifier: NCT05225428). Given the greater frequency of early-onset, aggressive PCs in patients with African ancestry, more data are needed in diverse populations. By design, all test results were disclosed by CGCs, and thus, postdisclosure surveys might have been influenced by these interactions, leading to potentially fewer differences between the two arms. Other considerations in this type of study design are the medical literacy of the patients, the design of the video, and the awareness and ability of GCs in determining and addressing participant literacy.[44] Educational attainment and literacy measures were not ascertained for trial participants. While the KnowGene scale was validated in women, this scale is applicable to multigene cancer panel testing and is pending further validation in more diverse patient populations with varied diagnoses. Analysis of cascade testing, impact on PC treatment, and somatic signatures for this cohort is in progress and will be reported separately.

Since the COVID-19 pandemic, there has been an expansion of virtual GC and implementation of technologies including chatbots and VE.[45-51] In 2021, leveraging the VE experience from this study, together with increasing GC referrals, the DFCI Division of Cancer Genetics and Prevention implemented clinical, in-person, VE service delivery. During the 18-month period of VE, 2,000 additional patients with cancer were served by this new workflow.

In conclusion, participants randomly assigned to VE or GC both had high levels of uptake of GT with high satisfaction. VE and other paradigms, which promote ease of GT of patients with PC and other cancers, will enable the identification of germline PVs with their downstream implications. However, nuanced differences between GC and VE exist and will be further studied and delineated in ongoing trials in diverse patient populations (ClinicalTrials.gov identifier: NCT04330716, NCT05225428).

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Pretest Video Education Versus Genetic Counseling for Patients With Prostate Cancer: A Multisite Randomized Controlled Trial

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APPENDIX. METHODS

Genes tested on CancerNext Expanded at the time of this study: *AIP*, *ALK*, *APC*, *ATM*, *BAP1*, *BARD1*, *BLM*, *BRCA1*, *BRCA2*, *BRIP1*, *BMPR1A*, *CDH1*, *CDK4*, *CDKN1B*, *CDKN2A*, *CHEK2*, *DICER1*, *EPCAM*, *FANCC*, *FH*, *FLCN*, *GALNT12*, *GREM1* (duplication/deletion only), *HOXB13*, *MAX*, *MEN1*, *MET*, *MITF* (p.E318K alteration only), *MLH1*, *MRE11A*, *MSH2*, *MSH6*, *MUTYH*, *NBN*, *NF1*, *NF2*, *PALB2*, *PHOX2B*, *PMS2*, *POLD1*, *POLE*, *POT1*, *PRKAR1A*, *PTCH1*, *PTEN*, *RAD50*, *RAD51C*, *RAD51D*, *RB1*, *RET*, *SDHA*, *SDHAF2*, *SDHB*, *SDHC*, *SDHD*, *SMAD4*, *SMARCA4*, *SMARCB1*, *SMARCE1*, *STK11*, *SUFU*, *TMEM127*, *TP53*, *TSC1*, *TSC2*, *VHL*, *XRCC2*.

Survey Measures

Result Disclosure Survey. The Result Disclosure Survey (RDS) analyzed whether the subject intended to share information about their genetic test results with family members.

Genetic Testing Satisfaction Survey. Answers to the Genetic Testing Satisfaction Survey (GTSS) ranged from disagree strongly to agree strongly on a 5-point Likert scale and were classified as either agree (agree and agree strongly) or disagree (disagree and disagree strongly), with neither agree nor disagree falling into the category that was considered less optimal depending on the question. For questions 1, 5, 7, and 8 "neither agree nor disagree" was grouped in the disagree category as this is the category of less desirable answers, and for questions 2, 3, 4, and 6 it was grouped in the agree category. A Fisher's exact test was used to test differences between arms for the RDS and the GTSS.

Multidimensional Impact of Cancer Risk Assessment. The Multidimensional Impact of Cancer Risk Assessment has been previously validated in men with *BRCA1/2* pathogenic variants (PVs)[34] and consists of questions split into three subscales: distress, uncertainty, and positive experiences.[35] Each subscale was scored, with the total score being the sum of the subscales. Answers were scored on a 0- to 3-point scale to conform with assumptions of the nonparametric test, subscales were scored if at most one question was unanswered in the subscale, and a total score was calculated only if all the subscales for that subject were available. Wilcoxon rank-sum tests were used to test for differences between arms. A Fisher's exact test was used to test for differences between the arms among participants with PVs on the Family Communication Survey, regarding result disclosure to relatives.

KnowGene. The KnowGene scale, a validated measure of knowledge of cancer multigene panel testing, was delivered 4 months after the result disclosure.[36] The number of questions correctly answered was summed for each participant and used as the outcome variable in a linear regression model with age at study entry (≤55, 55-65, and ≥65 years), random assignment arm (genetic counseling *v* video education), PV (*v* no PV), and metastatic prostate cancer (*v* nonmetastatic) as covariates.

TABLE A1. Summary Statistics for Difference Between 1-Month and 4-Month MICRA Total Scores

Total Score	Minimum	25%	Median	75%	Maximum	Mean	SD	IQR	*P*	% 0 Diff
VE										
PV (n = 36)	−16.0	−6.0	−1.0	3.0	9.0	−1.5	5.4	6.8	.15	8
No PV (n = 223)	−29.0	−6.0	−1.0	1.0	17.0	−2.1	6.1	5.3	<.001	8
GC										
PV (n = 12)	−4.0	−2.3	2.0	3.5	13.0	2.0	5.0	4.4	.34	0
No PV (n = 69)	−18.0	−6.0	−1.0	2.0	25.0	−1.6	6.8	6.0	.02	12
Distress subscale										
VE										
PV (n = 36)	−12.0	0	0	1.0	6.0	0.1	3.0	0.8	.45	47
No PV (n = 229)	−14.0	0	0	0	11.0	−0.4	2.3	0	.002	67
GC										
PV (n = 12)	−7.0	−0.3	0.5	3.3	6.0	1.0	3.4	2.7	.28	25
No PV (n = 72)	−7.0	0	0	0	12.0	−0.1	2.4	0	.51	65
Uncertainty subscale										
VE										
PV (n = 36)	−15.0	−1.3	0	2.2	5.0	−0.4	3.9	2.6	.69	31
No PV (n = 226)	−15.0	−2.0	0	2.0	15.0	−0.1	3.9	3.0	.69	21
GC										
PV (n = 12)	−3.0	−2.3	0.5	1.8	7.0	0.7	3.4	3.1	.62	8
No PV (n = 72)	−9.0	−1.0	0	2.0	14.0	0.2	4.1	2.3	.69	28
Positive experiences subscale										
VE										
PV (n = 36)	−10.0	−2.3	0	1.0	4.0	−1.3	3.5	2.5	.08	22
No PV (n = 229)	−12.0	−4.0	−1.0	0	12.0	−1.5	4.1	3.0	<.001	22
GC										
PV (n = 12)	−3.0	0	1.0	1.3	2.0	0.3	1.7	1.0	.62	25
No PV (n = 71)	−12.0	−4.0	−1.0	0	7.0	−1.7	4.1	3.0	<.001	24

NOTE. Summary statistics for difference between 1-month and 4-month MICRA scores had the following ranges: total score: possible range of −57 to 57; MICRA distress subscale scores, possible range of −18 to 18. MICRA uncertainty subscale scores, possible range of −27 to 27; positive experiences scale: possible range of −12 to 12.

Abbreviations: GC, genetic counseling; MICRA, Multidimensional Impact of Cancer Risk Assessment; PV, pathogenic variant; SD, standard deviation; VE, video education.

TABLE A2. Summary Statistics for the Number of Correct Answers on KnowGene by Covariate (possible range 0-24)

Covariate	Minimum	25th percentile	Median	75th percentile	Maximum	Mean	SD	IQR[a]	*P*
Age at study entry, years									
≤55	6	14	17	19	22	16.3	3.6	3.8	—
55-65	0	13	15	18	24	14.8	5.0	3.8	.07
≥65	0	13	15	18	23	15.1	4.2	3.8	.11
Random assignment									
GC	2	13	15	18	24	14.9	4.7	3.8	—
Video	0	13	16	18	23	15.2	4.3	3.8	.65
GT result									
No PV	0	13	16	18	24	15.2	4.4	3.8	—
PV	0	13	15.5	18	22	14.7	4.6	3.8	.45
PC disease status									
Metastatic	0	12	15	18	23	14.7	4.7	4.5	—
Nonmetastatic	0	13	16	18	24	15.4	4.2	3.8	.14

Abbreviations: GC, genetic counseling; GT, genetic test; PC, prostate cancer; PV, pathogenic variant; SD, standard deviation.
[a]IQR = (75th percentile − 25th percentile) × 0.75.

TABLE A3. Results Disclosure Survey

Response	Intent to Share (GC)	Intent to Share (VE)
No	1	5
Yes	130	446

Abbreviations: GC, genetic counseling; VE, video education.

TABLE A4. Family Communication Among Participants With PVs

Randomization arm	Did Not Tell Anyone	Told Someone
GC	0	12
VE	1	40

Abbreviations: GC, genetic counseling; PVs, pathogenic variants; VE, video education.